

10/525,743

Sequence Alignments

/JML/

RESULT 8  
AAP80269  
ID AAP80269 standard; protein; 212 AA.  
XX  
AC AAP80269;  
XX  
DT 15-JUN-2007 (revised)  
DT 25-MAR-2003 (revised)  
DT 03-OCT-2002 (revised)  
DT 08-OCT-1990 (first entry)  
XX  
DE Recombinant interleukin 6.  
XX  
KW IL-6; interleukin; cancer; BOND\_PC; interleukin 6 (interferon, beta 2);  
KW interleukin 6 (interferon, beta 2) [Homo sapiens]; IL6; HGF; HSF; BSF2;  
KW IL-6; IFNB2; interleukin 6 (interferon, beta 2), isoform CRA\_a;  
KW interleukin 6 (interferon, beta 2), isoform CRA\_a [Homo sapiens];  
KW unknown; unknown [Homo sapiens]; interleukin-6;  
KW interleukin-6 [Homo sapiens]; interferon 6 precursor; interleukin 6;  
KW hybridoma growth factor peptide; interleukin 6 [Homo sapiens];  
KW unnamed protein product; unnamed protein product [Homo sapiens];  
KW put. mature polypeptide (AA 1-184); IL6 [Homo sapiens];  
KW B cell stimulatory factor-2 (BSF-2);  
KW B cell stimulatory factor-2 (BSF-2) [Homo sapiens];  
KW interleukin 6 [synthetic construct];  
KW interleukin 6 (interferon, beta 2) [synthetic construct]; GO1781; GO5125;  
KW GO5138; GO5515; GO5576; GO5615; GO6953; GO6959; GO7166; GO7267; GO8284;  
KW GO8285; GO43066; GO45079; GO45630; GO45727.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .27  
FT /label= signal peptide  
FT Modified-site 73. .75  
FT /label= Glycosylation site  
FT /note= "N-linked"  
FT Modified-site 172. .174  
FT /label= Glycosylation site  
FT /note= "N-linked"  
XX  
PN WO8800206-A.  
XX  
PD 14-JAN-1988.  
XX  
PF 07-JUL-1987; 87WO-US001611.  
XX  
PR 08-JUL-1986; 86US-00883207.  
PR 15-JUL-1986; 86US-00885905.  
PR 08-MAY-1987; 87US-00047957.  
XX  
PA (GEMY ) GENETICS INST INC.

PI Clark SC, Wong GG, Schendel P, Mccoy J;  
XX  
DR WPI; 1988-021566/03.  
DR N-PSDB; AAN80299.  
DR PC:NCBI; gi|0834984.  
DR PC:SWISSPROT; P05231.  
DR PC:BIND; 116560,179493,116559,179102,262686,227104,179037.  
XX  
PT Prodn. of non-glycosylated IL-6 - for use in treatment of deficiency  
PT disorders in haematopoietic cells and in cancer therapy.  
XX  
PS Disclosure; Page ?; -pp; English.  
XX  
CC The sequence is encoded by DNA carried by pCSF309 in E.coli MC1061 (ATCC  
CC 67153) as an EcoRI insert. This can be excised and used to construct an  
CC expression plasmid for prodn. of IL-6. Bacterially produced IL-6 is non-  
CC glycosylated. It can be used against diseases caused by decreased levels  
CC of either myeloid or lymphoid cells of the haematopoietic system. It may  
CC also be used in conjunction with other interleukin therapies or as a  
CC hybridoma growth factor in culture medium. See also AAP80270. (Updated on  
CC 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct  
CC PR field.) (Updated on 25-MAR-2003 to correct PA field.)  
CC  
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
CC information from BOND.  
XX  
SQ Sequence 212 AA;

Query Match 94.7%; Score 790.5; DB 1; Length 212;  
Best Local Similarity 76.4%; Fred. No. 4.1e-73;  
Matches 162; Conservative 0; Mismatches 1; Indels 49; Gaps 1;

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Query Match      94.7%; Score 790.5; DB 1; Length 212;
Best Local Similarity 76.4%; Pred. No. 4.1e-73;
Matches 162; Conservative 0; Mismatches 1; Indels 49; Gaps 1;

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Qy 1 MNSFSTSAAFGPVAFLSLGLLVLPAAFFAPVPPGEDSKDVAAPHQRPLTSSERIDKQIRYI 60  
||| ||||| ||||| ||||| |||||  
Db 1 MNSFSTSAAFGPVAESLGLLVLPAAFFAPVPPGEDSKDVAAPHQRPLTSSERIDKQIRYI 60

Qy 61 LDGISALRKETCNKSNMCESSESKAELAENNPNLPKMAEKDGFQSGFNE----- 108  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 109 -----AKNLDAITTPDPTTNASLLTKLQ 131

Qy 132 AQNQWLQDMTHLILRSFKEFLQSSLRALRQM 163

Db 181 AQNQWLQDMTTHLILRSFKEFLQSSLRALRQM 212

### Alignment Scores:

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Pred. No.:          1.59e-73    Length:      212
Score:            790.50     Matches:      162
Percent Similarity: 76.4%   Conservative: 0
Best Local Similarity: 76.4%   Mismatches: 1
Query Match:       45.1%    Indels:      49
DB:                  1        Gaps:       1

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US-10-525-743A-2 (1-962) x AAP80269 (1-212)

Qy 34 ATGAACTCCTCTCCAAGCGCCTTCGGTCCAGTTGCCTTCCCTGGGCTGCTCCTG 93  
Db 1 MetAsnSerPheSerThrSerAlaPheGlyProValAlaPheSerLeuGlyLeuLeuLeu 20

Qy 94 GTGTTGCCTGCTGCCTCCCTGCCCAAGTACCCCCAGGAGAACAGATTCAAAGATGTAGCC 153  
Db 21 ValLeuProAlaAlaPheProAlaProValProProGlyGluAspSerLysAspValAla 40

Qy 154 GCCCCACACAGACAGCCACTCACCTTCAAGACGAATTGACAACAAATCGGTACATC 213  
Db 41 AlaProHisArgGlnProLeuThrSerSerGluArgIleAspLysGlnIleArgTyrIle 60

Qy 214 CTCGACGGCATCTCAGGCCCTGAGAAAAGGAGACATGTAACAAGAGTAACATGTGAAAGC 273  
Db 61 LeuAspGlyIleSerAlaLeuArgLysGluThrCysAsnLysSerAsnMetCysGluSer 80

Qy 274 AGCAAAGAGGCACTGGCAGAAAACACCGAACCTTCCAAGATGGCTGAAAAAGATGGA 333  
Db 81 SerLysGluAlaLeuAlaGluAsnAsnLeuAsnLeuProLysMetAlaGluLysAspGly 100

Qy 334 TGCTTCCAATCTGGATTCAATGAG----- 357  
Db 101 CysPheGlnSerGlyPheAsnGluGluThrCysLeuValLysIleIleThrGlyLeuLeu 120

Qy 357 ----- 357

Db 121 GluPheGluValTyrLeuGluTyrLeuGlnAsnArgPheGluSerSerGluGlnAla 140

Qy 358 -----GCAAAGAAT 366  
Db 141 ArgAlaValGlnMetSerThrLysValLeuIleGlnPheLeuGlnLysAlaLysAsn 160

Qy 367 CTAGATGCAATAACCACCCCTGACCCAACCAAAATGCCAGCCTGCTGACGAAAGCTGCAG 426  
Db 161 LeuAspAlaIleThrThrProAspProThrThrAsnAlaSerLeuLeuThrLysLeuGln 180

Qy 427 GCACAGAACAGTGGCTGCAGGACATGACAACACTCATCTCATCTGGCAGCTTAAGGAG 486  
Db 181 AlaGlnAsnGlnTrpLeuGlnAspMetThrThrHisLeuIleLeuArgSerPheGlu 200

Qy 487 TTCTGCAAGTCCAGCCTGAGGGCTCTCGGCAAATG 522  
Db 201 PheLeuGlnSerSerLeuArgAlaLeuArgGlnMet 212